

Application Serial No.: 10/037,922
Amendment dated: July 3, 2006
Response to Office Action dated May 2, 2006

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Amendments to the Specification:

Please replace the paragraph beginning on page 10, line 5 with the following amended paragraph:

Figure 1 and Figure 2 illustrate a multiple alignment of human fibroblast growth factor homologous factor 1 (FHF-1; SEQ ID NO:21), human myocyte-activating factor (FGF-10; SEQ ID NO: 22), human fibroblast growth factor homologous factor 4 (FHF-4; SEQ ID NO: 23), human fibroblast growth factor homologous factor 2 (FHF-2; SEQ ID NO: 24), human fibroblast growth factor homologous factor 3 (FHF-3; SEQ ID NO: 25), human FGF-4 (SEQ ID NO: 26), human FGF-6 (SEQ ID NO: 27), human FGF-2 (basic; SEQ ID NO: 28), human FGF-1 (acidic; SEQ ID NO:29), human keratinocyte growth factor 2 (KGF-2; SEQ ID NO: 30), human keratinocyte growth factor precursor (FGF-7; SEQ ID NO: 31), human zFGF-5 (SEQ ID NO:2), human FGF-8 (SEQ ID NO: 32), human FGF-5 (SEQ ID NO: 33), human FGF-9 (SEQ ID NO: 34), and human FGF-3 (SEQ ID NO: 35). "*" designates conserved amino acids; ":" designates conserved amino acid substitutions; and "." designates less stringently conserved amino acid substitutions.

Please replace the paragraph starting on page 14, line 16 with the following amended paragraph:

The novel zFGF-5 polypeptides of the present invention were initially identified by querying an EST database for growth factors. A single EST sequence was discovered and predicted to be related to the FGF family. The novel FGF homolog polypeptide encoded by the full length cDNA contained a motif of the formula: CXFXEX{6}Y (SEQ ID NO:36), wherein X is any amino acid and X{ } is the number of X amino acids greater than one. This motif occurs in all known members of the FGF family and is unique to these proteins.

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Please replace the paragraph starting on page 14, line 33 with the following amended paragraph:

The novel polypeptide encoded by the polynucleotide described herein contains the CXFXE{6}Y motif present in all members of the FGF family. The CXFXE{6}Y (SEQ ID NO: 36) motifs are highly conserved. A consensus amino acid sequence of the CXFXEX{6}Y (SEQ ID NO: 36) domain includes human fibroblast growth factor homologous factor 1 (FHF-1; Smallwood et al., Proc. Natl. Acad. Sci. USA 93:9850-9857, 1996), human myocyte-activating factor (FGF-10; HSU76381, GENBANK identifier, <http://www.ncbi.nlm.nih.gov/>), human fibroblast growth factor homologous factor 4 (FHF-4; Smallwood et al., 1996, *ibid.*), human fibroblast growth factor homologous factor 2 (FHF-2; Smallwood et al., 1996, *ibid.*), human fibroblast growth factor homologous factor 3 (FHF-3; Smallwood et al., 1996, *ibid.*), human FGF-4 (Basilico et al., Adv. Cancer Res. 59:115-165, 1992), human FGF-6 (Basilico et al., 1992, *ibid.*), human FGF-2 (basic; Basilico et al., 1992, *ibid.*), human FGF-1 (acidic; Basilico et al., 1992, *ibid.*), human keratinocyte growth factor 2 (KGF-2; HSU67918 GENBANK identifier, <http://www.ncbi.nlm.nih.gov/>), human keratinocyte growth factor precursor (FGF-7; Basilico et al., 1992, *ibid.*), human zFGF-5, human FGF-8 (Gemel et al., Genomics 35:253-257, 1996), human FGF-5 (Basilico et al., 1992, *ibid.*), human FGF-9 (Miyamoto et al., Mol. Cell. Biol. 13:4251-4259, 1993), and human FGF-3 (Basilico et al., 1992, *ibid.*)

Please replace the paragraph beginning on page 19, line 9 with the following amended paragraph:

The highly conserved amino acids in zFGF-5 can be used as a tool to identify new family members. To identify new family members in EST databases, the conserved CXFXEX{6}Y (SEQ ID NO: 36) motif can be used. In another method using polynucleotide probes and hybridization methods, RNA obtained from a variety of tissue sources can be used to generate cDNA libraries and probe these libraries for new family members. In particular, reverse transcription-polymerase chain reaction (RT-PCR) can be used to amplify sequences encoding highly degenerate DNA primers designed from the sequences corresponding to amino acid residue 127 (Cys) to amino acid residue 138(Tyr) of SEQ ID NO: 2.